

University of Groningen

Dynamic Modelling under Uncertainty

Achcar, Fiona; Kerkhoven, Eduard J.; SilicoTryp Consortium; Bakker, Barbara M.; Barrett, Michael P.; Breitling, Rainer

Published in:
 PLoS Computational Biology

DOI:
 [10.1371/journal.pcbi.1002352](https://doi.org/10.1371/journal.pcbi.1002352)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
 Publisher's PDF, also known as Version of record

Publication date:
 2012

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Achcar, F., Kerkhoven, E. J., SilicoTryp Consortium, Bakker, B. M., Barrett, M. P., & Breitling, R. (2012). Dynamic Modelling under Uncertainty: The Case of Trypanosoma brucei Energy Metabolism. *PLoS Computational Biology*, 8(1), [e1002352]. <https://doi.org/10.1371/journal.pcbi.1002352>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

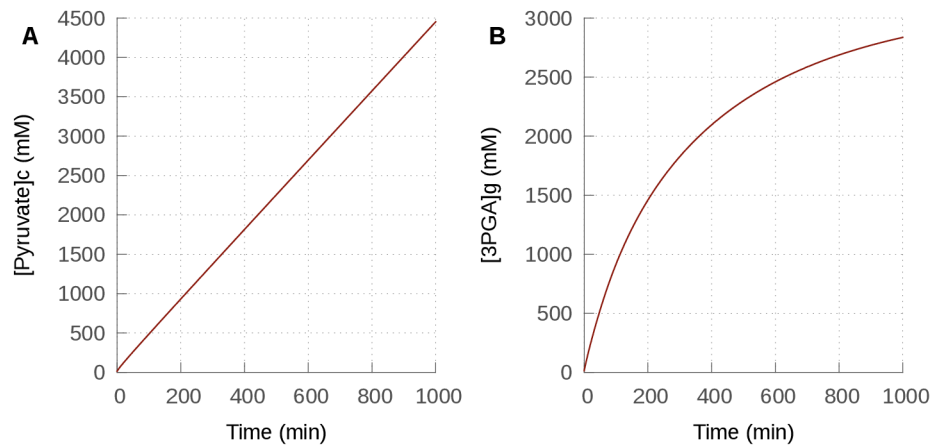


Figure S1.

Examples of simulations of models unable to reach steady-state (within 1000 simulated minutes). (A) Simulation of pyruvate concentration in a model unable to reach steady-state because of pyruvate accumulation. Models of this type will never reach steady-state. (B) Simulation of glycosomal 3-PGA concentration in a model unable to reach steady-state because of 3-PGA accumulation. Models of this type will eventually reach steady-state, but at extremely high concentrations of 3-PGA.